

## SEQUENCE LISTING

<110> Sheppard, Paul O.  
Baindur, Nand  
Bishop, Paul D.

<120> MAMMALIAN ADHESION PROTEASE PEPTIDES

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Arg Ala Arg Gly Thr Pro Leu  
10 15 20

102

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Trp Pro Val Pro Gly Ala Gly Val Leu Gln Gly His Ile Pro Gly Gln  
25 30 35

150

cca gtc acc ccg cac tgg gtc ctg gat gga caa ccc tgg cgc acc gtc  
Pro Val Thr Pro His Trp Val Leu Asp Gly Gln Pro Trp Arg Thr Val  
40 45 50

198

agc ctg gag gag ccg gtc tcg aag cca gac atg ggg ctg gtg gcc ctg	55	60	65	70	246
Ser Leu Glu Glu Pro Val Ser Lys Pro Asp Met Gly Leu Val Ala Leu					
gag gct gaa ggc cag gag ctc ctg ctt gag ctg gag aag aac cac agg	75	80	85		294
Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu Leu Glu Lys Asn His Arg					
ctg ctg gcc cca gga tac ata gaa acc cac tac ggc cca gat ggg cag	90	95	100		342
Leu Leu Ala Pro Gly Tyr Ile Glu Thr His Tyr Gly Pro Asp Gly Gln					
cca gtg gtg ctg gcc ccc aac cac acg gat cat tgc cac tac caa ggg	105	110	115		390
Pro Val Val Leu Ala Pro Asn His Thr Asp His Cys His Tyr Gln Gly					
cga gta agg ggc ttc ccc gac tcc tgg gta gtc ctc tgc acc tgc tct	120	125	130		438
Arg Val Arg Gly Phe Pro Asp Ser Trp Val Val Leu Cys Thr Cys Ser					
ggg atg agt ggc ctg atc acc ctc agc agg aat gcc agc tat tat ctg	135	140	145	150	486
Gly Met Ser Gly Leu Ile Thr Leu Ser Arg Asn Ala Ser Tyr Tyr Leu					
cgt ccc tgg cca ccc cgg ggc tcc aag gac ttc tca acc cac gag atc	155	160	165		534
Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp Phe Ser Thr His Glu Ile					
ttt cgg atg gag cag ctg ctc acc tgg aaa gga acc tgt ggc cac agg	170	175	180		582
Phe Arg Met Glu Gln Leu Leu Thr Trp Lys Gly Thr Cys Gly His Arg					
gat cct ggg aac aaa gcg ggc atg acc agc ctt cct ggt ggt ccc cag	185	190	195		630
Asp Pro Gly Asn Lys Ala Gly Met Thr Ser Leu Pro Gly Gly Pro Gln					
agc agg ggc agg cga gaa gcg cgc agg acc cgg aag tac ctg gaa ctg	200	205	210		678
Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr Arg Lys Tyr Leu Glu Leu					
tac att gtg gca gac cac acc ctg ttc ttg act cgg cac cga aac ttg	215	220	225	230	726
Tyr Ile Val Ala Asp His Thr Leu Phe Leu Thr Arg His Arg Asn Leu					

aac cac acc aaa cag cgt ctc ctg gaa gtc gcc aac tac gtg gac cag			774
Asn His Thr Lys Gln Arg Leu Leu Glu Val Ala Asn Tyr Val Asp Gln			
235	240	245	
ctt ctc agg act ctg gac att cag gtg gcg ctg acc ggc ctg gag gtg			822
Leu Leu Arg Thr Leu Asp Ile Gln Val Ala Leu Thr Gly Leu Glu Val			
250	255	260	
tgg acc gag cgg gac cgc agc cgc gtc acg cag gac gcc aac gcc acg			870
Trp Thr Glu Arg Asp Arg Ser Arg Val Thr Gln Asp Ala Asn Ala Thr			
265	270	275	
ctc tgg gcc ttc ctg cag tgg cgc cgg ggg ctg tgg gcg cag cgg ccc			918
Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly Leu Trp Ala Gln Arg Pro			
280	285	290	
cac gac tcc gcg cag ctg ctc acg ggc cgc gcc ttc cag ggc gcc aca			966
His Asp Ser Ala Gln Leu Leu Thr Gly Arg Ala Phe Gln Gly Ala Thr			
295	300	305	310
gtg ggc ctg gcg ccc gtc gag ggc atg tgc cgc gcc gag agc tcg gga			1014
Val Gly Leu Ala Pro Val Glu Gly Met Cys Arg Ala Glu Ser Ser Gly			
315	320	325	
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Gly Val Ser Thr Asp His Ser Glu Leu Pro Ile Gly Ala Ala Ala Thr			
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atg gcc cat gag atc ggc cac agc ctc ggc ctc agc cac gac ccc gac			1110
Met Ala His Glu Ile Gly His Ser Leu Gly Leu Ser His Asp Pro Asp			
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Gly Cys Cys Val Glu Ala Ala Ala Glu Ser Gly Gly Cys Val Met Ala			
360	365	370	
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Ala Ala Thr Gly His Pro Phe Pro Arg Val Phe Ser Ala Cys Ser Arg			
375	380	385	390

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Asn Ala Pro Asp Pro Gly Leu Pro Val Pro Ala Leu Cys Gly Asn			
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Gly Phe Val Glu Ala Gly Glu Glu Cys Asp Cys Gly Pro Gly Gln Glu			
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Cys Arg Asp Leu Cys Cys Phe Ala His Asn Cys Ser Leu Arg Pro Gly			
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Ala Gln Cys Ala His Gly Asp Cys Cys Val Arg Cys Leu Leu Lys Pro			
455	460	465	470
gct gga gcg ctg tgc cgc cag gcc atg ggt gac tgt gac ctc cct gag			1494
Ala Gly Ala Leu Cys Arg Gln Ala Met Gly Asp Cys Asp Leu Pro Glu			
475	480	485	
ttt tgc acg ggc acc tcc tcc cac tgt ccc cca gac gtt tac cta ctg			1542
Phe Cys Thr Gly Thr Ser Ser His Cys Pro Pro Asp Val Tyr Leu Leu			
490	495	500	
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Asp Gly Ser Pro Cys Ala Arg Gly Ser Gly Tyr Cys Trp Asp Gly Ala			
505	510	515	
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Cys Pro Thr Leu Glu Gln Gln Cys Gln Gln Leu Trp Gly Pro Gly Ser			
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His Pro Ala Pro Glu Ala Cys Phe Gln Val Val Asn Ser Ala Gly Asp			
535	540	545	550
gct cat gga aac tgc ggc cag gac agc gag ggc cac ttc ctg ccc tgt			1734
Ala His Gly Asn Cys Gly Gln Asp Ser Glu Gly His Phe Leu Pro Cys			
555	560	565	

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Pro	Ser	Leu	Leu	Ala	Pro	His	Met	Val	Pro	Val	Asp	Ser	Thr	Val	His	
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Leu	Asp	Gly	Gln	Glu	Val	Thr	Cys	Arg	Gly	Ala	Leu	Ala	Leu	Pro	Ser	
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gcc	cag	ctg	gac	ctg	ctt	ggc	ctg	ggc	ctg	gta	gag	cca	ggc	acc	cag	1926
Ala	Gln	Leu	Asp	Leu	Leu	Gly	Leu	Gly	Leu	Val	Glu	Pro	Gly	Thr	Gln	
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Phe	Gln	Glu	Leu	Gln	Arg	Cys	Leu	Thr	Ala	Cys	His	Ser	His	Gly	Ala	
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Val	Ala	Leu	Cys	Arg	Leu	Lys	Thr	Met	Thr	Pro	Ser	Cys	Trp	Pro	Cys	
680						685									690	
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Ser	Ser	Ala	Ser	Cys	Cys	Leu	Cys	Ser	Gln	Gly	Pro	Ala	Trp	Pro	Gly	
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gtt	gct	acc	gac	tcc	cag	gag	ccc	atc	tgc	agc	gat	gca	gct	ggg	gct	2214
Val	Ala	Thr	Asp	Ser	Gln	Glu	Pro	Ile	Cys	Ser	Asp	Ala	Ala	Gly	Ala	
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gcc acc ctg aga agc ctc tgc cag cag tct cgc ctg acc ccc aag atc Ala Thr Leu Arg Ser Leu Cys Gln Gln Ser Arg Leu Thr Pro Lys Ile 775 780 785 790	2406
aag tcc aga tgc caa gat cct gcc tct ggt gag agg tagtcctaa Lys Ser Arg Cys Gln Asp Pro Ala Ser Gly Glu Arg 795 800	2452
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 35 40 45  
 Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp  
 50 55 60  
 Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu  
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 Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His  
 85 90 95  
 Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Asp  
 100 105 110  
 His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp Val  
 115 120 125  
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 145 150 155 160  
 Phe Ser Thr His Glu Ile Phe Arg Met Glu Gln Leu Leu Thr Trp Lys  
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 Gly Thr Cys Gly His Arg Asp Pro Gly Asn Lys Ala Gly Met Thr Ser  
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 Arg Lys Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe Leu  
 210 215 220  
 Thr Arg His Arg Asn Leu Asn His Thr Lys Gln Arg Leu Leu Glu Val  
 225 230 235 240  
 Ala Asn Tyr Val Asp Gln Leu Leu Arg Thr Leu Asp Ile Gln Val Ala  
 245 250 255  
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 260 265 270  
 Gln Asp Ala Asn Ala Thr Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly  
 275 280 285  
 Leu Trp Ala Gln Arg Pro His Asp Ser Ala Gln Leu Leu Thr Gly Arg  
 290 295 300  
 Ala Phe Gln Gly Ala Thr Val Gly Leu Ala Pro Val Glu Gly Met Cys  
 305 310 315 320  
 Arg Ala Glu Ser Ser Gly Gly Val Ser Thr Asp His Ser Glu Leu Pro  
 325 330 335



Leu Val Ala Ala Trp Thr Val Ala Leu Cys Arg Leu Lys Thr Met Thr  
 675 680 685  
 Pro Ser Cys Trp Pro Cys Ser Ser Ala Ser Cys Cys Leu Cys Ser Gln  
 690 695 700  
 Gly Pro Ala Trp Pro Gly Val Ala Thr Asp Ser Gln Glu Pro Ile Cys  
 705 710 715 720  
 Ser Asp Ala Ala Gly Ala Ala Glu Gly Thr Leu Arg Ala Val Ala Pro  
 725 730 735  
 Lys Met Ala His Thr Gly Thr Pro Trp Ala Ala Phe Thr Pro Trp  
 740 745 750  
 Ser Trp Ala Pro Gln Pro Leu Asp Ser Pro Gly Pro Trp Thr Leu Arg  
 755 760 765  
 Thr Leu Met Ser Pro Ala Ala Thr Leu Arg Ser Leu Cys Gln Gln Ser  
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 Trp Pro Val Pro Gly Ala Gly Val Leu Gln Gly His Ile Pro Gly Gln  
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Pro Val Thr Pro His Trp Val Leu Asp Gly Gln Pro Trp Arg Thr Val			
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Ser Leu Glu Glu Pro Val Ser Lys Pro Asp Met Gly Leu Val Ala Leu			
55	60	65	70
gag gct gaa ggc cag gag ctc ctg ctt gag ctg gag aag aac cac agg			294
Glu Ala Glu Gly Gln Glu Leu Leu Glu Leu Glu Lys Asn His Arg			
75	80	85	
ctg ctg gcc cca gga tac ata gaa acc cac tac ggc cca gat ggg cag			342
Leu Leu Ala Pro Gly Tyr Ile Glu Thr His Tyr Gly Pro Asp Gly Gln			
90	95	100	
cca gtg gtg ctg gcc ccc aac cac acg gat cat tgc cac tac caa ggg			390
Pro Val Val Leu Ala Pro Asn His Thr Asp His Cys His Tyr Gln Gly			
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Arg Val Arg Gly Phe Pro Asp Ser Trp Val Val Leu Cys Thr Cys Ser			
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Gly Met Ser Gly Leu Ile Thr Leu Ser Arg Asn Ala Ser Tyr Tyr Leu			
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cgt ccc tgg cca ccc cgg ggc tcc aag gac ttc tca acc cac gag atc			534
Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp Phe Ser Thr His Glu Ile			
155	160	165	
ttt cgg atg gag cag ctg ctc acc tgg aaa gga acc tgt ggc cac agg			582
Phe Arg Met Glu Gln Leu Leu Thr Trp Lys Gly Thr Cys Gly His Arg			
170	175	180	
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Asp Pro Gly Asn Lys Ala Gly Met Thr Ser Leu Pro Gly Gly Pro Gln			
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Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr Arg Lys Tyr Leu Glu Leu			
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Tyr Ile Val Ala Asp His Thr Leu Phe Leu Thr Arg His Arg Asn Leu		
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Asn His Thr Lys Gln Arg Leu Leu Glu Val Ala Asn Tyr Val Asp Gln		
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Leu Leu Arg Thr Leu Asp Ile Gln Val Ala Leu Thr Gly Leu Glu Val		
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Trp Thr Glu Arg Asp Arg Ser Arg Val Thr Gln Asp Ala Asn Ala Thr		
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His Asp Ser Ala Gln Leu Leu Thr Gly Arg Ala Phe Gln Gly Ala Thr		
295 300 305 310		
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Val Gly Leu Ala Pro Val Glu Gly Met Cys Arg Ala Glu Ser Ser Gly		
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Gly Val Ser Thr Asp His Ser Glu Leu Pro Ile Gly Ala Ala Ala Thr		
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atg gcc cat gag atc ggc cac agc ctc ggc ctc agc cac gac ccc gac		1110
Met Ala His Glu Ile Gly His Ser Leu Gly Leu Ser His Asp Pro Asp		
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Gly Cys Cys Val Glu Ala Ala Glu Ser Gly Gly Cys Val Met Ala		
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gct	gcc	acc	ggg	cac	ccg	ttt	ccg	cgc	gtg	ttc	agc	gcc	tgc	agc	cgc	1206
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Asn	Ala	Pro	Asp	Pro	Gly	Leu	Pro	Val	Pro	Pro	Ala	Leu	Cys	Gly	Asn	
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Gly	Phe	Val	Glu	Ala	Gly	Glu	Glu	Cys	Asp	Cys	Gly	Pro	Gly	Gln	Glu	
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Cys	Arg	Asp	Leu	Cys	Cys	Phe	Ala	His	Asn	Cys	Ser	Leu	Arg	Pro	Gly	
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gct	gga	gct	tgc	cgc	cag	gcc	atg	ggt	gac	tgt	gac	ctc	cct	gag		1494
Ala	Gly	Ala	Leu	Cys	Arg	Gln	Ala	Met	Gly	Asp	Cys	Asp	Leu	Pro	Glu	
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Phe	Cys	Thr	Gly	Thr	Ser	Ser	His	Cys	Pro	Pro	Asp	Val	Tyr	Leu	Leu	
490				495					500							
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Asp	Gly	Ser	Pro	Cys	Ala	Arg	Gly	Ser	Gly	Tyr	Cys	Trp	Asp	Gly	Ala	
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Cys	Pro	Thr	Leu	Glu	Gln	Gln	Cys	Gln	Gln	Leu	Trp	Gly	Pro	Gly	Ser	
520				525					530							
cac	cca	gct	ccc	gag	gcc	tgt	ttc	cag	gtg	gtg	aac	tct	gct	gga	gat	1686
His	Pro	Ala	Pro	Glu	Ala	Cys	Phe	Gln	Val	Val	Asn	Ser	Ala	Gly	Asp	
535				540					545				550			

gct cat gga aac tgc ggc cag gac agc gag ggc cac ttc ctg ccc tgt			1734
Ala His Gly Asn Cys Gly Gln Asp Ser Glu Gly His Phe Leu Pro Cys			
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gca ggg agg gat gcc ctg tgt ggg aag ctg cag tgc cag ggt gga aag			1782
Ala Gly Arg Asp Ala Leu Cys Gly Lys Leu Gln Cys Gln Gly Gly Lys			
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Pro Ser Leu Leu Ala Pro His Met Val Pro Val Asp Ser Thr Val His			
585	590	595	
cta gat ggc cag gaa gtg act tgt cgg gga gcc ttg gca ctc ccc agt			1878
Leu Asp Gly Gln Glu Val Thr Cys Arg Gly Ala Leu Ala Leu Pro Ser			
600	605	610	
gcc cag ctg gac ctg ctt ggc ctg ggc ctg gta gag cca ggc acc cag			1926
Ala Gln Leu Asp Leu Leu Gly Leu Gln Leu Val Glu Pro Gly Thr Gln			
615	620	625	630
tgt gga cct aga atg gtg tgc cag agc agg cgc tgc agg aag aat gcc			1974
Cys Gly Pro Arg Met Val Cys Gln Ser Arg Arg Cys Arg Lys Asn Ala			
635	640	645	
ttc cag gag ctt cag cgc tgc act gcc tgc cac agc cac ggg gtt			2022
Phe Gln Glu Leu Gln Arg Cys Leu Thr Ala Cys His Ser His Gly Val			
650	655	660	
tgc aat agc aac cat aac tgc cac tgt gct cca ggc tgg gct cca ccc			2070
Cys Asn Ser Asn His Asn Cys His Cys Ala Pro Gly Trp Ala Pro Pro			
665	670	675	
ttc tgt gac aag cca ggc ttt ggt ggc agc atg gac agt ggc cct gtg			2118
Phe Cys Asp Lys Pro Gly Phe Gly Gly Ser Met Asp Ser Gly Pro Val			
680	685	690	
cag gct gaa aac cat gac acc ttc ctg ctg gcc atg ctc ctc agc gtc			2166
Gln Ala Glu Asn His Asp Thr Phe Leu Leu Ala Met Leu Leu Ser Val			
695	700	705	710

ctg ctg cct ctg ctc cca ggg gcc ggc ctg gcc tgg tgt tgc tac cga Leu Leu Pro Leu Leu Pro Gly Ala Gly Leu Ala Trp Cys Cys Tyr Arg 715 720 725	2214
ctc cca gga gcc cat ctg cag cga tgc agc tgg ggc tgc aga agg gac Leu Pro Gly Ala His Leu Gln Arg Cys Ser Trp Gly Cys Arg Arg Asp 730 735 740	2262
cct gcg tgc agt ggc ccc aaa gat ggc cca cac agg gac cac ccc ctg Pro Ala Cys Ser Gly Pro Lys Asp Gly Pro His Arg Asp His Pro Leu 745 750 755	2310
ggc ggc gtt cac ccc atg gag ttg ggc ccc aca gcc act gga cag ccc Gly Gly Val His Pro Met Glu Leu Gly Pro Thr Ala Thr Gly Gln Pro 760 765 770	2358
tgg ccc ctg gac cct gag aac tct cat gag ccc agc agc cac cct gag Trp Pro Leu Asp Pro Glu Asn Ser His Glu Pro Ser Ser His Pro Glu 775 780 785 790	2406
aag cct ctg cca gca gtc tcg cct gac ccc caa gat caa gtc cag atg Lys Pro Leu Pro Ala Val Ser Pro Asp Pro Gln Asp Gln Val Gln Met 795 800 805	2454
cca aga tcc tgc ctc tgg tgagaggtag ctcctaaaat gaacagattt Pro Arg Ser Cys Leu Trp 810	2502
aaagacaggt ggccactgac agccactcca ggaacttcaa ctgcagggc agagccagtg aatcaccgga cctccagcac ctgcaggcag cttggaaagtt tcttccccga gtggagcttc gacccaccca ctccaggaac ccagagccac attagaagtt cctgagggtggct ggagaacact gctggcaca ctctccagct caataaacca tcagtcccag aagcaaaggt cacacagccc ctgacccccc tcaccagtgg aggctggta gtgtggcca tcccaaaagg gctctgtcct gggagtctgg tgtgtctcct acatgcaatt tccacggacc cagctctgtg gagggcatga ctgctggcca gaagctgtg gtcctgggc cctatggtc gactgagtcc acactccct ggagcctggc tggcctctgc aaacaaacat aattttgggg accttccttc ctgtttcttc ccaccctgtc ttctccctt ggtggttcct gagccccac ccccaatccc agtgcac ctgaggttct ggagctcaga atctgacagc ctctccccc ttctgtgtgt gtcgggggaa cagagggAAC catttaagaa aagataccaa agtagaaagtc aaaagaaaga catgttgct ataggcgtgg tggctcatgc ctataatccc agcactttgg gaagccgggg taggaggatc accagaggcc agcaggtcca caccagcctg ggcaacacag caagacaccg catctacaga aaaattttaa aattagctgg gcgtgggtgt gtgtacctgt aggccttagct gctcaggagg ctgaagcagg aggatcactt gagcctgagt tcaacactgc agtgagctat ggtggcacca	2562 2622 2682 2742 2802 2862 2922 2982 3042 3102 3162 3222 3282 3342 3402

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atatta 3468

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<213> Homo sapiens

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20 25 30  
Gly His Ile Pro Gly Gln Pro Val Thr Pro His Trp Val Leu Asp Gly  
35 40 45  
Gln Pro Trp Arg Thr Val Ser Leu Glu Glu Pro Val Ser Lys Pro Asp  
50 55 60  
Met Gly Leu Val Ala Leu Glu Ala Glu Gly Gln Glu Leu Leu Leu Glu  
65 70 75 80  
Leu Glu Lys Asn His Arg Leu Leu Ala Pro Gly Tyr Ile Glu Thr His  
85 90 95  
Tyr Gly Pro Asp Gly Gln Pro Val Val Leu Ala Pro Asn His Thr Asp  
100 105 110  
His Cys His Tyr Gln Gly Arg Val Arg Gly Phe Pro Asp Ser Trp Val  
115 120 125  
Val Leu Cys Thr Cys Ser Gly Met Ser Gly Leu Ile Thr Leu Ser Arg  
130 135 140  
Asn Ala Ser Tyr Tyr Leu Arg Pro Trp Pro Pro Arg Gly Ser Lys Asp  
145 150 155 160  
Phe Ser Thr His Glu Ile Phe Arg Met Glu Gln Leu Leu Thr Trp Lys  
165 170 175  
Gly Thr Cys Gly His Arg Asp Pro Gly Asn Lys Ala Gly Met Thr Ser  
180 185 190  
Leu Pro Gly Gly Pro Gln Ser Arg Gly Arg Arg Glu Ala Arg Arg Thr  
195 200 205  
Arg Lys Tyr Leu Glu Leu Tyr Ile Val Ala Asp His Thr Leu Phe Leu  
210 215 220  
Thr Arg His Arg Asn Leu Asn His Thr Lys Gln Arg Leu Leu Glu Val  
225 230 235 240  
Ala Asn Tyr Val Asp Gln Leu Leu Arg Thr Leu Asp Ile Gln Val Ala  
245 250 255  
Leu Thr Gly Leu Glu Val Trp Thr Glu Arg Asp Arg Ser Arg Val Thr  
260 265 270

Gln Asp Ala Asn Ala Thr Leu Trp Ala Phe Leu Gln Trp Arg Arg Gly  
 275 280 285  
 Leu Trp Ala Gln Arg Pro His Asp Ser Ala Gln Leu Leu Thr Gly Arg  
 290 295 300  
 Ala Phe Gln Gly Ala Thr Val Gly Leu Ala Pro Val Glu Gly Met Cys  
 305 310 315 320  
 Arg Ala Glu Ser Ser Gly Gly Val Ser Thr Asp His Ser Glu Leu Pro  
 325 330 335  
 Ile Gly Ala Ala Ala Thr Met Ala His Glu Ile Gly His Ser Leu Gly  
 340 345 350  
 Leu Ser His Asp Pro Asp Gly Cys Cys Val Glu Ala Ala Glu Ser  
 355 360 365  
 Gly Gly Cys Val Met Ala Ala Ala Thr Gly His Pro Phe Pro Arg Val  
 370 375 380  
 Phe Ser Ala Cys Ser Arg Arg Gln Leu Arg Ala Phe Phe Arg Lys Gly  
 385 390 395 400  
 Gly Gly Ala Cys Leu Ser Asn Ala Pro Asp Pro Gly Leu Pro Val Pro  
 405 410 415  
 Pro Ala Leu Cys Gly Asn Gly Phe Val Glu Ala Gly Glu Cys Asp  
 420 425 430  
 Cys Gly Pro Gly Gln Glu Cys Arg Asp Leu Cys Cys Phe Ala His Asn  
 435 440 445  
 Cys Ser Leu Arg Pro Gly Ala Gln Cys Ala His Gly Asp Cys Cys Val  
 450 455 460  
 Arg Cys Leu Leu Lys Pro Ala Gly Ala Leu Cys Arg Gln Ala Met Gly  
 465 470 475 480  
 Asp Cys Asp Leu Pro Glu Phe Cys Thr Gly Thr Ser Ser His Cys Pro  
 485 490 495  
 Pro Asp Val Tyr Leu Leu Asp Gly Ser Pro Cys Ala Arg Gly Ser Gly  
 500 505 510  
 Tyr Cys Trp Asp Gly Ala Cys Pro Thr Leu Glu Gln Gln Cys Gln Gln  
 515 520 525  
 Leu Trp Gly Pro Gly Ser His Pro Ala Pro Glu Ala Cys Phe Gln Val  
 530 535 540  
 Val Asn Ser Ala Gly Asp Ala His Gly Asn Cys Gly Gln Asp Ser Glu  
 545 550 555 560  
 Gly His Phe Leu Pro Cys Ala Gly Arg Asp Ala Leu Cys Gly Lys Leu  
 565 570 575  
 Gln Cys Gln Gly Gly Lys Pro Ser Leu Leu Ala Pro His Met Val Pro  
 580 585 590  
 Val Asp Ser Thr Val His Leu Asp Gly Gln Glu Val Thr Cys Arg Gly  
 595 600 605

Ala Leu Ala Leu Pro Ser Ala Gln Leu Asp Leu Leu Gly Leu Gly Leu  
 610 615 620  
 Val Glu Pro Gly Thr Gln Cys Gly Pro Arg Met Val Cys Gln Ser Arg  
 625 630 635 640  
 Arg Cys Arg Lys Asn Ala Phe Gln Glu Leu Gln Arg Cys Leu Thr Ala  
 645 650 655  
 Cys His Ser His Gly Val Cys Asn Ser Asn His Asn Cys His Cys Ala  
 660 665 670  
 Pro Gly Trp Ala Pro Pro Phe Cys Asp Lys Pro Gly Phe Gly Ser  
 675 680 685  
 Met Asp Ser Gly Pro Val Gln Ala Glu Asn His Asp Thr Phe Leu Leu  
 690 695 700  
 Ala Met Leu Leu Ser Val Leu Leu Pro Leu Leu Pro Gly Ala Gly Leu  
 705 710 715 720  
 Ala Trp Cys Cys Tyr Arg Leu Pro Gly Ala His Leu Gln Arg Cys Ser  
 725 730 735  
 Trp Gly Cys Arg Arg Asp Pro Ala Cys Ser Gly Pro Lys Asp Gly Pro  
 740 745 750  
 His Arg Asp His Pro Leu Gly Gly Val His Pro Met Glu Leu Gly Pro  
 755 760 765  
 Thr Ala Thr Gly Gln Pro Trp Pro Leu Asp Pro Glu Asn Ser His Glu  
 770 775 780  
 Pro Ser Ser His Pro Glu Lys Pro Leu Pro Ala Val Ser Pro Asp Pro  
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<210> 5

<211> 2406

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<213> Artificial Sequence

<220>

<223> Degenerate sequence

<221> misc\_feature

<222> (1)...(2406)

<223> n = A,T,C or G

<400> 5

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acnccncayt	gggtynytna	yggncarccn	tggmgnacng	tnwsnytna	rgarccngtn	180

wsnaarccng	ayatggnyt	ngtngcnytn	gargcngarg	gncargaryt	nytnytngar	240
ytngaraara	aycaymgnyt	nytngcnccn	ggnayathg	aracncayta	yggncncngay	300
ggncarccng	tngtnytngc	nccnaaycay	acngaycayt	gycaytayca	rggnmgngtn	360
mgnggnttyc	cngaywsntg	ggtngtnytn	tgyacntgyw	snggnatgws	nggnytnath	420
acnytnwsnm	gnaaygcnws	ntaytayytn	mgncntggc	cnccnmngg	nwsnaargay	480
ttywsnacnc	aygarathtt	ymgnatggar	carytnytna	cntggaargg	nacntgyggn	540
caymngayc	cnggnaayaa	rgcnggnatg	acnwsnytnc	cnggnggncc	ncarwsnmgn	600
ggnmgnmng	argcnmgnmg	nacnmgnaar	tayytngary	tntayathgt	ngcngaycay	660
acnytnttyy	tnacnmgnca	ymgnnaayytn	aaycayacna	arcarmgnyt	nytngargtn	720
gcnaaytag	tngaycaryt	nytnmgnacn	ytngayathc	argtngcnyt	nacnggnytn	780
gargtntgga	cngarmgnga	ymgnwsnmgn	gtacncarg	aygcnaaygc	nacnytntrgg	840
gcnttuytnc	artggmgnmg	nggnytntrgg	gcncarmgncc	cncaygayws	ngcncarytn	900
ytnacnggnm	gngcnttyca	rggngcnacn	gtnggnytn	cnccngtna	rggnatgtgy	960
mgngcngarw	snwsngngg	ngtrwsnacn	gaycaywsng	arytnccnat	hggngcngcn	1020
gcnaacnatgg	cncaygarat	hggncaywsn	ytnggnytnw	sncaygaycc	ngayggntgy	1080
tgygtngarg	cngcngcnga	rwsngnggn	tgygtnatgg	cngcngcnac	nggnacayccn	1140
ttyccnmng	tnttywsngc	ntgywsnmgn	mgnacarytnm	gngcnttuyt	ymgnnaarggn	1200
gnggngcnt	gyytnwsnaa	ycnccngay	ccnggnytnc	cngtncncc	ngcnytntrgy	1260
gnaayggnt	tygtngargc	ngngargar	tgygaytgyg	gnccnggnca	rgartgymgn	1320
gayytntrgyt	gyttrgcnca	yaaytgywsn	ytnmgnccng	gngcncartg	ycnccaygg	1380
gaytgytgyg	tnmgntgyyt	nytnaarcn	gcngngcny	tntgymgnca	rgcнатgggn	1440
gaytgygavy	tnccngartt	ytgyacnggn	acnwsnwsnc	aytgyccncc	ngaygtntay	1500
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acnytnarc	arcartgyca	rcarytntrgg	ggncnggnw	sncayccncc	ncncargcn	1620
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gncayttryy	tnccntgygc	nggnmgnay	gncnytntrgyg	gnaarytnca	rtgycarggn	1740
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acnggnacna	cnccntggc	ngcnttuyt	ccntggwsnt	gggcncnca	rccnytnay	2280
wsnccngngc	cntggacnyt	nmgnaacnytn	atgwsnccng	cngcnaacnyt	nmgnsnytn	2340
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garmgn						2406

&lt;210&gt; 6

&lt;211&gt; 2439

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

018

&lt;220&gt;

&lt;223&gt; Degenerate sequence

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(2439)

&lt;223&gt; n = A,T,C or G

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acnccncayt gggtnytna	yggncarccn tggmgnacng	tnwsnytna rgarcnngt	180
wsnaarccng ayatgggnyt	ngtngcnytn gargcngarg	gncargaryt nytnytngar	240
ytnbaraara aycaymgnyt	nytngcnccn ggntayathg	aracncayta yggncnngay	300
ggncarccng tngtnytngc	nccnaaycay acngaycayt	gycaytayca rggmgnngt	360
mgnggnnttgc cngaywsntg	ggtngtnytn tgyacntgyw	snggnatgws nggnynath	420
acnytrwsnm gnaaygcnws	ntaytaytn mgnccntggc	cnccnmgnng nwsnaargay	480
ttywsnacnc aygarathtt	ymgnatggar carytnytna	cntggaargg nacntgyggn	540
caymngngayc cnggnaayaa	rgcnggnatg acnwsnytnc	cnggngncc ncarwsnmgn	600
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gcnaaytayg tngaycaryt	nytnmgnacn ytnayathc	argtngcnyt nacnggnyn	780
gargtntgca cngarmngna	ymgnwsnmgn gtnacncarg	aygcnaaygc nacnytnntgg	840
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ggnccnccnacnacnacn	gnccnggnca rgartgymgn	ggnccnccnacnacnacn	2040

gayaarccng gnttyggngg nwsnatggay wsnggnccng tncargcnga raaycaygay	2100
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<223> oligonucleotide ZC17,993

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<223> Oligonucleotide API

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<210> 17  
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<400> 17  
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<210> 18  
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<210> 19  
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<210> 20  
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<212> DNA  
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<220>  
<223> oligonucleotide ZC20,646

<400> 20  
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<210> 21  
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<220>  
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<400> 21  
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<210> 22  
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<223> oligonucleotide ZC20,633

<400> 22  
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<210> 23  
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<220>  
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<210> 24  
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<210> 25  
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<220>  
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<210> 26  
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<220>

<223> oligonucleotide ZC21,075

<400> 26

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18

105